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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:40:16 : Search time 12.47 Seconds
(without alignments)
39.701 Million cell updates/sec

Title: US-08-940-096-146

Perfect score: 105

Sequence: 1 PVLEFLEFLEFLEFLLDALQKLLK 22

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 132412

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PTCUTS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	105	100.0	22 3	US-08-940-095-146 Sequence 146, App
2	105	100.0	22 3	US-08-940-095-174 Sequence 174, App
3	105	100.0	22 3	US-08-940-093-146 Sequence 146, App
4	105	100.0	22 3	US-08-940-093-174 Sequence 174, App
5	105	100.0	22 3	US-08-940-096-146 Sequence 146, App
6	105	100.0	22 3	US-08-940-096-174 Sequence 174, App
7	105	100.0	22 4	US-09-465-719-146 Sequence 146, App
8	105	100.0	22 4	US-09-465-719-174 Sequence 174, App
9	102	97.1	22 3	US-08-940-095-150 Sequence 150, App
10	102	97.1	22 3	US-08-940-095-159 Sequence 159, App
11	102	97.1	22 3	US-08-940-095-169 Sequence 169, App
12	102	97.1	22 3	US-08-940-095-179 Sequence 179, App
13	102	97.1	22 3	US-08-940-095-188 Sequence 188, App
14	102	97.1	22 3	US-08-940-093-150 Sequence 150, App
15	102	97.1	22 3	US-08-940-093-159 Sequence 159, App
16	102	97.1	22 3	US-08-940-093-169 Sequence 169, App
17	102	97.1	22 3	US-08-940-093-179 Sequence 179, App
18	102	97.1	22 3	US-08-940-093-188 Sequence 188, App
19	102	97.1	22 3	US-08-940-096-150 Sequence 150, App
20	102	97.1	22 3	US-08-940-096-159 Sequence 159, App
21	102	97.1	22 3	US-08-940-096-169 Sequence 169, App
22	102	97.1	22 3	US-08-940-096-179 Sequence 179, App
23	102	97.1	22 3	US-08-940-096-188 Sequence 188, App
24	102	97.1	22 4	US-09-465-719-150 Sequence 150, App
25	102	97.1	22 4	US-09-465-719-159 Sequence 159, App
26	102	97.1	22 4	US-09-465-719-169 Sequence 169, App
27	102	97.1	22 4	US-09-465-719-179 Sequence 179, App

28	102	97.1	22 4	US-09-465-719-188 Sequence 188, App
29	101	96.2	22 3	US-08-940-095-147 Sequence 147, App
30	101	96.2	22 3	US-08-940-095-152 Sequence 152, App
31	101	96.2	22 3	US-08-940-095-157 Sequence 157, App
32	101	96.2	22 3	US-08-940-095-161 Sequence 161, App
33	101	96.2	22 3	US-08-940-093-147 Sequence 147, App
34	101	96.2	22 3	US-08-940-093-152 Sequence 152, App
35	101	96.2	22 3	US-08-940-093-157 Sequence 157, App
36	101	96.2	22 3	US-08-940-096-147 Sequence 147, App
37	101	96.2	22 3	US-08-940-096-152 Sequence 152, App
38	101	96.2	22 3	US-08-940-096-157 Sequence 157, App
39	101	96.2	22 3	US-08-940-096-161 Sequence 161, App
40	101	96.2	22 4	US-09-465-719-147 Sequence 147, App
41	101	96.2	22 4	US-09-465-719-152 Sequence 152, App
42	101	96.2	22 4	US-09-465-719-157 Sequence 157, App
43	101	96.2	22 4	US-09-465-719-161 Sequence 161, App
44	101	96.2	22 3	US-08-940-095-165 Sequence 165, App
45	100	95.2	22 3	US-08-940-095-165 Sequence 165, App

ALIGNMENTS

RESULT 1
US-08-940-095-146
Sequence 146, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-146

Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLLEFENLERLLDALOKKIK 22
Db 1 PVLLEFENLERLLDALOKKIK 22

RESULT 2

US-08-940-095-174

; Sequence 174 Application US/08940095
; Patent No. 6004925

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095

FILING DATE: 29-SEP-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A

REGISTRATION NUMBER: 30,742

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 174:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. 6004925e
FEATURE:

NAME/KEY: Other
LOCATION: 1...22

OTHER INFORMATION: All amino acids are in the D-configuration

US-08-940-095-174

Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLLEFENLERLLDALOKKIK 22
Db 1 PVLLEFENLERLLDALOKKIK 22

RESULT 3

US-08-940-093-146

; Sequence 146 Application US/08940093
; Patent No. 6037323

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.093

FILING DATE: 29-SEP-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A

REGISTRATION NUMBER: 30,742

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. 6037323e

US-08-940-093-146

Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLLEFENLERLLDALOKKIK 22
Db 1 PVLLEFENLERLLDALOKKIK 22

RESULT 4

US-08-940-093-174

; Sequence 174 Application US/08940093
; Patent No. 6037323

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258

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TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE: NAME/KEY: Other
LOCATION: 1...22
OTHER INFORMATION: All amino acids are in the D-configuration
US-08-940-096-174

Query Match
Best Local Similarity 100.0%; Score 105; DB 3; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PVELEFENLERLDAOKK 22
DB 1 PVELEFENLERLDAOKK 22

RESULT 7
US-09-465-719-146
Sequence 146 Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESSES:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cotruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION: 009196-0006-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE: NAME/KEY: Other
LOCATION: 1...22
OTHER INFORMATION: All amino acids are in the D-configuration
US-09-465-719-174

US-09-465-719-146

Query Match
Best Local Similarity 100.0%; Score 105; DB 4; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PVELEFENLERLDAOKK 22
DB 1 PVELEFENLERLDAOKK 22

RESULT 8
US-09-465-719-174
Sequence 174 Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESSES:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cotruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION: 009196-0006-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE: NAME/KEY: Other
LOCATION: 1...22
OTHER INFORMATION: All amino acids are in the D-configuration
US-09-465-719-174

Query Match
Best Local Similarity 100.0%; Score 105; DB 4; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PVELEFENLERLDAOKK 22
DB 1 PVELEFENLERLDAOKK 22

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RESULT 9
US-08-940-095-150
Sequence 150, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-150

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0;

OY 1 PVLLEFENLERLDALOKKIK 22
DB 1 PVLLEFENLERLDALOKKIK 22

RESULT 10
US-08-940-095-159
Sequence 159, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS: Pennie & Edmonds LLP
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-159

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0;

OY 1 PVLLEFENLERLDALOKKIK 22
DB 1 PVLLEFENLERLDALOKKIK 22

RESULT 11
US-08-940-095-169
Sequence 169, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELEPHONE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-169

Query Match
Best Local Similarity 97.1%; Score 102; DB 3; Length 22;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLELFENLERLDAALOKKLK 22
DB 1 PVLELFENLERLDAALOKKLK 22

RESULT 12
US-08-940-095-179
Sequence 179; Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELEPHONE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-188

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-179

Query Match
Best Local Similarity 97.1%; Score 102; DB 3; Length 22;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLELFENLERLDAALOKKLK 22
DB 1 PVLELFENLERLDAALOKKLK 22

RESULT 13
US-08-940-095-188
Sequence 188; Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELEPHONE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-188

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PYLELFENLERLIDALOKK 22
1 PYLELFENLERLIDALOKK 22
DB 1 PYLELFENLERLIDALOKK 22

RESULT 14
US-08-940-093-150
Sequence 150, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-150

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PYLELFENLERLIDALOKK 22
1 PYLELFENLERLIDALOKK 22
DB 1 PYLELFENLERLIDALOKK 22

RESULT 15
US-08-940-093-159
Sequence 159, Application US/08940093
Patent No. 6037323

GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-159

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PYLELFENLERLIDALOKK 22
1 PYLELFENLERLIDALOKK 22
DB 1 PYLELFENLERLIDALOKK 22

Search completed: November 20, 2001, 09:43:25
Job time: 189 sec

Tue Nov 20 10:24:50 2001

us-08-940-096-146.nov20.ra1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:39:15 : Search time 17.78 Seconds
(without alignments)
75.013 Million cell updates/sec

Title: US-08-940-096-146
Perfect score: 1 PVLLEFENLERLDAIQKKLK 22
Sequence:

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 187964

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_0601: *
2: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT: *
3: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT: *
4: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT: *
5: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT: *
6: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT: *
7: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT: *
8: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT: *
9: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT: *
10: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT: *
11: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT: *
12: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT: *
13: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT: *
14: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT: *
15: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT: *
16: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT: *
17: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT: *
18: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT: *
19: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT: *
20: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT: *
21: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT: *
22: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	22	AAV19107	Lecithin:cholester
2	105	100.0	22	AAV19079	Lecithin:cholester
3	105	100.0	22	AAV18853	Lecithin:cholester
4	105	100.0	22	AAV18825	Lecithin:cholester
5	105	100.0	22	AAV18590	Lecithin:cholester
6	105	100.0	22	AAV18562	Lecithin:cholester
7	105	100.0	22	AAV19361	Lecithin:cholester
8	105	100.0	22	AAV19333	Lecithin:cholester
9	102	97.1	22	AAV19375	Lecithin:cholester
10	102	97.1	22	AAV19346	Lecithin:cholester
11	102	97.1	22	AAV19356	Lecithin:cholester

12	102	97.1	22	AAV19112	Lecithin:cholester
13	102	97.1	22	AAV19121	Lecithin:cholester
14	102	97.1	22	AAV19102	Lecithin:cholester
15	102	97.1	22	AAV19083	Lecithin:cholester
16	102	97.1	22	AAV19092	Lecithin:cholester
17	102	97.1	22	AAV18858	Lecithin:cholester
18	102	97.1	22	AAV18867	Lecithin:cholester
19	102	97.1	22	AAV18848	Lecithin:cholester
20	102	97.1	22	AAV18829	Lecithin:cholester
21	102	97.1	22	AAV18838	Lecithin:cholester
22	102	97.1	22	AAV18595	Lecithin:cholester
23	102	97.1	22	AAV18604	Lecithin:cholester
24	102	97.1	22	AAV18575	Lecithin:cholester
25	102	97.1	22	AAV18585	Lecithin:cholester
26	102	97.1	22	AAV18566	Lecithin:cholester
27	102	97.1	22	AAV19366	Lecithin:cholester
28	102	97.1	22	AAV19337	Lecithin:cholester
29	101	96.2	22	AAV19344	Lecithin:cholester
30	101	96.2	22	AAV19348	Lecithin:cholester
31	101	96.2	22	AAV19080	Lecithin:cholester
32	101	96.2	22	AAV19085	Lecithin:cholester
33	101	96.2	22	AAV19090	Lecithin:cholester
34	101	96.2	22	AAV19094	Lecithin:cholester
35	101	96.2	22	AAV18826	Lecithin:cholester
36	101	96.2	22	AAV18831	Lecithin:cholester
37	101	96.2	22	AAV18836	Lecithin:cholester
38	101	96.2	22	AAV18840	Lecithin:cholester
39	101	96.2	22	AAV18577	Lecithin:cholester
40	101	96.2	22	AAV18563	Lecithin:cholester
41	101	96.2	22	AAV18568	Lecithin:cholester
42	101	96.2	22	AAV19334	Lecithin:cholester
43	101	96.2	22	AAV19339	Lecithin:cholester
44	101	96.2	22	AAV19352	Lecithin:cholester
45	100	95.2	22	AAV19352	Lecithin:cholester

ALIGNMENTS

RESULT 1	
AAV19107	standard; Peptide: 22 AA.
AC	AAV19107;
XX	
DT	09-JUL-1999 (first entry)
XX	
DE	Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.
XX	
XX	Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW	human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
KW	cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW	high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW	septic shock.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FN	W09916458-A1.
XX	
PD	08-APR-1999.
XX	
PF	28-SEP-1998; 98WO-US20326.
XX	
PR	29-SEP-1997; 97US-0940096.
XX	
PA	(BUTN) BUTNER K.
PA	(CORN) CORNUT I.
PA	(DASS) DASSEUX J.
PA	(METZ) METZ G.
XX	(SEKU) SEKUL R.
PI	Butner K, Cornut I, Dasseux J, Metz G, Sekul R;

XX DR WPI, 1999-277034/23.
XX

XX PT Peptide agonists of apolipoprotein A-I
XX

XX PS Example; Page 116; 254pp; English.
XX

CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoa-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoa-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoa-I agonists.
XX

XX Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKIK 22
DB 1 PVLELFENLERLIDALQKKIK 22

RESULT 2

AAI19079
ID AAY19079 standard; Peptide: 22 AA.

AC AAY19079;

DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.

KW Apolipoprotein A-I; agonist: dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoa-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.

XX Synthetic.

OS Homo sapiens.

XX WO916458-A1.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20326.

XX 29-SEP-1997; 97US-0940096.

XX (BUTL/) BUTTNER K.

XX (CORN/) CORNUT I.

XX (DASS/) DASSEUX J.

XX (METZ/) METZ G.

XX (SEKU/) SEKUL R.

XX Butner K, Cornut I, Dasseux J, Metz G, Sekul R;

XX WPI, 1999-277034/23.

XX Peptide agonists of apolipoprotein A-I

XX Claim 18; Page 115; 254pp; English.

XX

CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoa-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoa-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoa-I agonists.
XX

XX Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKIK 22
DB 1 PVLELFENLERLIDALQKKIK 22

RESULT 3

AAI18853
ID AAY18853 standard; Peptide: 22 AA.

AC AAY18853;

DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.

KW Apolipoprotein A-I; agonist: dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoa-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.

XX Synthetic.

OS Homo sapiens.

XX WO916408-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20328.

XX 29-SEP-1997; 97US-0940093.

XX (BUTL/) BUTTNER K.

XX (CORN/) CORNUT I.

XX (DASS/) DASSEUX J.

XX (METZ/) METZ G.

XX (SEKU/) SEKUL R.

XX Butner K, Cornut I, Dasseux J, Metz G, Sekul R;

XX WPI, 1999-277031/23.

XX Peptide agonists of apolipoprotein A-I

XX Example; Page 113; 152pp; English.

XX The present invention describes an agonist (A) of apolipoprotein A-I

XX (apoa-I) which is a 14-22 residue peptide, or analog, that forms an

XX amphipathic alpha-helix in presence of lipids. (A), and their lipid

XX complexes, are used to treat or prevent diseases associated with

XX dyslipidemia, specifically hypercholesterolaemia, cardiovascular

CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to
 CC AAY18933 represent lecitin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLDALOKKLK 22
 1 PVLELFENLERLDALOKKLK 22

RESULT 4
 AAY18825
 ID AAY18825 standard; Peptide: 22 AA.

AC AAY18825;
 DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.

XX Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.

XX Synthetic.
 OS Homo sapiens.

XX MO9916408-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20328.

XX 29-SEP-1997; 97US-0940093.

XX (BUTN/) BUTTNER K.
 XX (CORN/) CORNUT I.
 XX (DASS/) DASSEUX J.
 XX (METZ/) METZ G.
 XX (SEKU/) SEKUL R.

PI Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;

XX WPI: 1999-277031/23.

XX Peptide agonists of apolipoprotein A-I

XX Example: Page 112; 152pp; English.

CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to

CC AAY18933 represent lecitin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLDALOKKLK 22
 1 PVLELFENLERLDALOKKLK 22

RESULT 5
 AAY18590
 ID AAY18590 standard; Peptide: 22 AA.

AC AAY18590;

DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.

XX Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

XX Synthetic.
 OS Homo sapiens.

XX MO9916409-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20329.

XX 29-SEP-1997; 97US-0940136.

XX (BUTN/) BUTTNER K.
 XX (CORN/) CORNUT I.
 XX (DASS/) DASSEUX J.
 XX (DUFO/) DUFOURCQ J.
 XX (METZ/) METZ G.
 XX (SEKU/) SEKUL R.

PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
 PI Sekul R;

XX WPI: 1999-254921/21.

XX Nucleic acid encoding apolipoprotein A-I agonist peptides

XX Example: Page 178; 232pp; English.

CC The present invention describes a nucleic acid (A) encoding an
 CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents a peptide from the present invention.

XX Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKLK 22
Db 1 pvllelfenlerlidaqlqkik 22

RESULT 6
AAV18562

ID AAV18562 standard; Peptide; 22 AA.

AC AAV18562;

DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.

KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

OS Synthetic.

OS Homo sapiens.

PN W09916409-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20329.

PR 29-SEP-1997; 97US-0940136.

PA (BUTN/) BUTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (DUFO/) DUFOURCO J.

PA (METZ/) METZ G.

PA (SEKUL/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R;

WPI: 1999-254921/21.

Nucleic acid encoding apolipoprotein A-I agonist peptides

Claim 35; Page 170; 232pp; English.

The present invention describes a nucleic acid (A) encoding an apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog, which forms an amphipathic alpha-helix in presence of lipids. (A), optionally as a complex with lipids, and host cells that contain (A), are useful for gene therapy, or prevention, of diseases associated with dyslipidemia, specifically hypercholesterolemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to study the role of apoA-I in lipid metabolism. (B) can be used diagnostically, e.g. to measure serum HDL (particularly its subpopulation involved in retrograde cholesterol transport) and for imaging the circulatory system or HDL accumulations at fatty streaks. The present sequence represents a peptide from the present invention.

Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3e-08;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKLK 22
Db 1 pvllelfenlerlidaqlqkik 22

RESULT 7
AAV19361

ID AAV19361 standard; Peptide; 22 AA.

AC AAV19361;

DT 14-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.

KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.

OS Synthetic.

OS Homo sapiens.

PN W09916459-A1.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20327.

PR 29-SEP-1997; 97US-0940095.

PA (BUTN/) BUTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (DUFO/) DUFOURCO J.

PA (METZ/) METZ G.

PA (SEKUL/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R;

WPI: 1999-277035/23.

Peptide agonists of apolipoprotein A-I

Example; Page 125; 280pp; English.

The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAV19188 to AAV19441 represent lecithin:cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists.

Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3e-08;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKLK 22

Db 1 pvllelfenlerlidaqlqkik 22

XX Lecithin:cholesterol acyltransferase activation exhibiting peptide #159.
 DE Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 XX human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 XX high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 XX septic shock.

OS Synthetic.
 OS Homo sapiens.

XX MO9916459-A1.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20327.

XX 29-SEP-1997; 97US-0940095.

XX (BUTT/) BUTTNER K.

XX (CORN/) CORNUT I.

XX (DASS/) DASSEUX J.

XX (DUFO/) DUFOURCQ J.

XX (METZ/) METZ G.

XX (SEKU/) SEKUL R.

XX Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

XX Sekul R;

XX WPI: 1999-277035/23.

XX Peptide agonists of apolipoprotein A-I

XX Example; Page 124; 280pp; English.

XX The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL. In particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAV19188 to
 CC AAV19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA;

Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLELFENLRLDALQKRLK 22
 DB 1 pvllelfenlrlldalqkrlk 22

RESULT 11

AAV19356
 ID AAV19356 standard; Peptide; 22 AA.

AC AAV19356;

XX 14-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #169.

XX Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW septic shock.

KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 XX septic shock.

OS Synthetic.
 OS Homo sapiens.

XX MO9916459-A1.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20327.

XX 29-SEP-1997; 97US-0940095.

XX (BUTT/) BUTTNER K.

XX (CORN/) CORNUT I.

XX (DASS/) DASSEUX J.

XX (DUFO/) DUFOURCQ J.

XX (METZ/) METZ G.

XX (SEKU/) SEKUL R.

XX Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

XX Sekul R;

XX WPI: 1999-277035/23.

XX Peptide agonists of apolipoprotein A-I

XX Example; Page 125; 280pp; English.

XX The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL. In particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAV19188 to
 CC AAV19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA;

Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLELFENLRLDALQKRLK 22
 DB 1 pvllelfenlrlldalqkrlk 22

RESULT 12

AAV19112
 ID AAV19112 standard; Peptide; 22 AA.

AC AAV19112;

XX 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #179.

XX Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.

XX OS Synthetic.
XX OS Homo sapiens.
XX MO9916458-A1.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US20326.
XX PR 29-SEP-1997; 97US-0940096.
XX PA (BUTT/) BUTTNER K.
XX PA (CORN/) CORNUT I.
XX PA (DASS/) DASSEUX J.
XX PA (METZ/) METZ G.
XX PA (SEKU/) SEKUL R.
XX PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;
XX PS WPI: 1999-277034/23.
XX DR Peptide agonists of apolipoprotein A-I
XX PT Example: Page 116; 254pp: English.
XX PS The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAV18934 to AAV19187 represent lecitin:cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA:
Query Match 97.1%; Score 102; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 6e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVELFENLRLDALQKRLK 22
Db 1 pvelfentlrlldalqkrlk 22

RESULT 13
AAV19121
ID AAV19121 standard; Peptide: 22 AA.
XX AAV19121;
XX DT 09-JUL-1999 (first entry)
XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #188.
XX KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN MO9916458-A1.
XX

PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US20326.
XX PR 29-SEP-1997; 97US-0940096.
XX PA (BUTT/) BUTTNER K.
XX PA (CORN/) CORNUT I.
XX PA (DASS/) DASSEUX J.
XX PA (METZ/) METZ G.
XX PA (SEKU/) SEKUL R.
XX PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;
XX PS WPI: 1999-277034/23.
XX DR Peptide agonists of apolipoprotein A-I
XX PT Claim 18; Page 117; 254pp: English.
XX PS The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAV18934 to AAV19187 represent lecitin:cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA:
Query Match 97.1%; Score 102; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 6e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVELFENLRLDALQKRLK 22
Db 1 pvelfentlrlldalqkrlk 22

RESULT 14
AAV19102
ID AAV19102 standard; Peptide: 22 AA.
XX AAV19102;
XX DT 09-JUL-1999 (first entry)
XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #169.
XX KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN MO9916458-A1.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US20326.
XX PR 29-SEP-1997; 97US-0940096.
XX

P	I	Buttner K, Cornut I, Dasseux J, Metz G, Sekul R:
X	X	WPI; 1999-277034/23.
D	R	
X	X	Peptide agonists of apolipoprotein A-I
P	T	
PS		Claim 18; Page 115; 254pp; English.
XX		
CC,		The present invention describes an agonist (A) of apolipoprotein A-I
CC,		(apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC		amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC		complexes, are used to treat or prevent diseases associated with
CC		dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC		disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC		apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC		treating septic shock. When labeled, (A) can also be used diagnostically
CC		to measure serum levels of HDL, in particular the HDL subpopulation that
CC		is involved in retrograde cholesterol transport, also to image HDL at
CC		e.g. atherosclerotic streaks, and to raise antibodies. AA18934 to
CC		AA19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC		exhibiting core peptides, which are apoA-I agonists.
XX		
SQ		Sequence 22 AA;
		Query Match 97.1%; Score 102; DB 20; Length 22;
		Best Local Similarity 95.5%; Pred. No. 6e-08;
		Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Query Match          97.1%;   Score 102;   DB 20;   Length 22;
Best Local Similarity 95.5%;   Pred. No. 6e-08; 0;   Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0;

Oy      1 PVLELFENLIERLLDALOKRLK 22
        |:|:|||||:|||||:|
Db      1 plllelfenllerlldalqkklk 22

Search completed: November 20, 2001, 09:43:06
Job time: 231 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2001, 09:41:06 ; Search time 12.74 Seconds
(without alignments)
131.542 Million cell updates/sec

Title: US-08-940-096-146
Perfect score: 105
Sequence: 1 PYLEPFLNLERLDALQKKLK 22

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 6208

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	33.3	26	2	H64589
2	32	30.5	24	2	B48368
3	31.5	30.0	29	2	B85840
4	31.5	30.0	29	2	C85840
5	31	29.5	21	1	A35225
6	31	29.5	30	1	OEON2K
7	25.7	25.7	24	2	T43971
8	25.7	25.7	25	2	PC4445
9	25.7	25.7	26	2	PL0027
10	24.8	24.8	24	2	A20554
11	24.8	24.8	24	2	G20554
12	24.8	24.8	24	2	H20554
13	24.8	24.8	26	2	S62672
14	26	24.8	26	2	S02788
15	26	24.8	28	2	A23691
16	26	24.8	30	2	H70152
17	25	23.8	26	2	F20554
18	25	23.8	29	2	S51070
19	25	23.8	29	2	CS4037
20	25	23.8	29	2	A49410
21	24	22.9	14	2	S13864
22	24	22.9	16	2	S65709
23	24	22.9	20	2	C20554
24	24	22.9	23	4	A58505
25	24	22.9	25	2	D20554
26	24	22.9	25	2	G41606
27	24	22.9	26	1	B57082
28	24	22.9	27	1	SEBO
29	24	22.9	27	1	SESH

ALIGNMENTS

30	24	22.9	27	2	A44641	homeotic protein H
31	23	21.9	14	2	I51430	hemoglobin beta ch
32	23	21.9	20	2	S63602	glutathione S-tran
33	23	21.9	22	2	I58038	MHC class I transp
34	23	21.9	22	2	A37335	68k surface anti
35	23	21.9	23	2	A33948	glutathione trans
36	23	21.9	24	2	A45336	cystic fibrosis tr
37	23	21.9	24	2	I39680	exer protein - Aer
38	23	21.9	24	2	B27262	nicotinic acetylch
39	23	21.9	26	1	LESAD	delta hemolysin -
40	23	21.9	26	2	A40630	hypothetical prote
41	23	21.9	26	2	F69265	hypothetical prote
42	23	21.9	26	4	I55277	hemoglobin alpha c
43	23	21.9	27	1	S07443	secretin - human
44	23	21.9	27	2	A27267	secretin - dog
45	23	21.9	27	2	C60415	secretin - rabbit

RESULT 1
H64589
hypothetical protein (HP0560, jhp0507) - Helicobacter pylori
C:Species: Helicobacter pylori
A:Variety: strains J99, 26695
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: H64589; A71923
R:Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKee,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: H64589
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <TOM>
A:Cross-references: GB:AE000570; GB:AE000511; NID:q2313672; PIDN:AAD0633.1; PID:q231
A:Experimental source: strain 26695
R:Alm, R.A.; Ling, L.S.L.; Molt, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.
; Ives, C.; Gibson, R.; Meberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:97120537
A:Accession: A71923
A:Molecule type: DNA
A:Residues: 1-26 <ARN>
A:Cross-references: GB:AE001484; GB:AE001439; NID:q4155043; PIDN:AAD06083.1; PID:q415
A:Experimental source: strain J99
C:Genetics:
A:Gene: HP0560; jhp0507

Query Match 33.3%; Score 35; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 97;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 LERLDAIQQK 20
DB 15 LAYRIIDVLEQK 26

RESULT 2
B48368
N5,N10-methylethyltetrahydromethanopterin cyclohydrolase - Methanosarcina barkeri (Fragm
C:Species: Methanosarcina barkeri
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B48368
R:Klein, A.R.; Breitung, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.
Arch. Microbiol. 159, 213-219, 1993
A:Title: N5,N10-methylethyltetrahydromethanopterin cyclohydrolase from the extremely the

from the extremely thermophilic *Methanopyrus kandleri*.
 A:Reference number: A48368; MUID:93243882

A:Contents: Fusaro D
 A:Accession: B48368

A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-24 <KLE>

A:Note: sequence extracted from NCBI backbone (NCBIP:130470)

Query Match 30.5%; Score 32; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 VLEFENLERLDAQ 16
 | | | | | | | | | | | | | | | | | |
 Db 4 VNEGMSNVIEMLDS 18

RESULT 3
 B85840
 hypothetical protein Z3289 [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

A:Accession: B85840

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85840

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-29 <STO>

A:Cross-references: GB:AE005174; NID:g12516340; PIDN:AGS7182.1; GSPDB:GN00145; UWGP:232

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z3289

Query Match 30.0%; Score 31.5; DB 2; Length 29;
 Best Local Similarity 58.8%; Pred. No. 3.4e+02;
 Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 2 VLEFENLERLDAQ 18
 | | | | | | | | | | | | | | | | | |
 Db 14 VLELLVALL-RLIDLK 29

RESULT 4
 C85840
 hypothetical protein Z3290 [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

A:Accession: C85840

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C85840

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-29 <STO>

A:Cross-references: GB:AE005174; NID:g12516341; PIDN:AGS7183.1; GSPDB:GN00145; UWGP:232

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z3290

OY 2 VLEFENLERLDAQ 18
 | | | | | | | | | | | | | | | | | |
 Db 14 VLELLVALL-RLIDLK 29

RESULT 5
 A35225
 conantokin T - cone shell (*Conus tulipa*)

N:Alternate names: sleeper peptide

C:Species: *Conus tulipa* (tulip cone)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A:Accession: A35225

R:Haack, J.A.; Rivier, J.; Parks, T.N.; Mena, E.E.; Cruz, L.J.; Olivera, B.M.

J. Biol. Chem. 265, 6025-6029, 1990

A:Title: Conantokin-T, A gamma-carboxyglutamate containing peptide with N-methyl-D-as

A:Reference number: A35225; MUID:90202866

A:Accession: A35225

A:Molecule type: protein

A:Residues: 1-2, 'XX', 5-9, 'X', 11-13, 'X', 15-21 <HAA>

A:Note: the residues designated 'X' were determined to be gamma-carboxy glutamic acid

C:Comment: This venom peptide induces sleep in young mice and is an NMDA antagonist 1

C:Superfamily: conantokin

C:Keywords: amidated carboxyl end; carboxyglutamic acid; neurotoxin; venom

F:3,4,10,14/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental

F:21/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 29.5%; Score 31; DB 1; Length 21;
 Best Local Similarity 41.2%; Pred. No. 2.8e+02;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 4 ELPENLERLDAQ 20
 | | | | | | | | | | | | | | | | | |
 Db 3 EBYQKMLENLEAEVKK 19

RESULT 6
 OEON2K
 beta-endorphin II - chum salmon

N:Contains: Met-enkephalin

C:Species: *Oncorhynchus keta* (chum salmon)

C:Date: 31-May-1980 #sequence_revision 31-May-1980 #text_change 21-Jan-2000

A:Accession: A01469

R:Kawauchi, H.; Tsubokawa, M.; Kanazawa, A.; Kitagawa, H.

Biochem. Biophys. Res. Commun. 92, 1278-1288, 1980

A:Title: Occurrence of two different endorphins in the salmon pituitary.

A:Reference number: A01469; MUID:80174902

A:Accession: A01469

A:Molecule type: protein

A:Residues: 1-30 <KAW>

C:Superfamily: corticotropin-lipotropin

C:Keywords: acetylated amino end; opioide peptide

F:1-5/Product: Met-enkephalin #status predicted <MEN>

F:1/Modified site: acetylated amino end (Tyr) #status experimental

Query Match 29.5%; Score 31; DB 1; Length 30;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 PVLEFENL 10
 | | | | | | | | | | | | | | | | | |
 Db 15 PLTLFKNVI 24

RESULT 7
 T43971
 CC-chemokine receptor [imported] - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6

A:Variety: strain HST

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T43971

R;Iseigawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kaw
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: 222732; MUID:99412319
A:Accession: T43971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <ISE>
A:Cross-references: EMBL:AB021506; NID:g4959597; PIN:BA78232.1; PID:g4959599
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U12

Query Match 25.7%; Score 27; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 LERLLDALOKK 21
| : | : | : | : |
Db 7 LSKLLVSIQRSL 18

RESULT 8
PCA445
L-ascorbate peroxidase (EC 1.11.1.11) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Mar-1998 #sequence_revision 08-May-1998 #text_change 07-May-1999
C:Accession: PCA445
R:Mada, N.; Kinoshita, S.; Matsuo, M.; Amako, K.; Miyake, C.; Asada, K.
Biochem. Biophys. Res. Commun. 242, 256-261, 1998
A:Title: Purification and molecular properties of ascorbate peroxidase from bovine eye.
A:Reference number: PCA445; MUID:98113338
A:Accession: PCA445
A:Molecule type: protein
A:Residues: 1-25 <MAD>
C:Comment: This hydrogen peroxide-scavenging peroxidase plays a role in the protection
C:Keywords: oxidoreductase

Query Match 25.7%; Score 27; DB 2; Length 25;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLELFEN 8
: | | | | |
Db 15 IKELFEN 21

RESULT 9
PL0027
M protein pepM19 - Streptococcus sp. (fragment)
C:Species: Streptococcus sp.
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Feb-1997
C:Accession: PL0027
R:Bronze, M.S.; Beachey, E.H.; Dale, J.B.
J. Exp. Med. 167, 1849-1859, 1988
A:Title: Protective and heart-crossreactive epitopes located within the NH2 terminus of
A:Reference number: PL0027; MUID:88258373
A:Accession: PL0027
A:Molecule type: Protein
A:Residues: 1-26 <BRO>
C:Superfamily: M5 protein
C:Keywords: virulence factor

Query Match 25.7%; Score 27; DB 2; Length 26;
Best Local Similarity 35.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 7 ENLLELLDALOKK 20
| : | : | : | : |
Db 9 EDKLRKIIDLDAK 22

RESULT 10
A20554
hemocyanin subunit I - Atlantic horseshoe crab (fragment)
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 12-Apr-1995
C:Accession: A20554
R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiard, P.; Jolles, P.; Jolles, J.; Feldmann,
Biochemistry 22, 5573-5583, 1983
A:Title: Quaternary structure of Limulus polyphemus hemocyanin.
A:Reference number: A90478
A:Accession: A20554
A:Molecule type: protein
A:Residues: 1-24 <LAM>
C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunit
C:Superfamily: hemocyanin

Query Match 24.8%; Score 26; DB 2; Length 24;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLELFENI 9
: | | | | : |
Db 9 ILALFEHL 16

RESULT 11
G20554
hemocyanin subunit V - Atlantic horseshoe crab (fragment)
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 08-Jul-1994
C:Accession: G20554
R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiard, P.; Jolles, P.; Jolles, J.; Feldmann,
Biochemistry 22, 5573-5583, 1983
A:Title: Quaternary structure of Limulus polyphemus hemocyanin.
A:Reference number: A90478
A:Accession: G20554
A:Molecule type: protein
A:Residues: 1-24 <LAM>
C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunit

Query Match 24.8%; Score 26; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 LLDALOKK 22
: | | | | : |
Db 1 VLSVLQKLR 10

RESULT 12
H20554
hemocyanin subunit VI - Atlantic horseshoe crab (fragment)
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 08-Jul-1994
C:Accession: H20554
R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiard, P.; Jolles, P.; Jolles, J.; Feldmann,
Biochemistry 22, 5573-5583, 1983
A:Title: Quaternary structure of Limulus polyphemus hemocyanin.
A:Reference number: A90478
A:Accession: H20554
A:Molecule type: protein
A:Residues: 1-24 <LAM>
C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunit

Query Match 24.8%; Score 26; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 13 LLDALOKKLR 22
 :| | | :
 Db 1 VLGALEKOLR 10

RESULT 13

S62672
 transcobalamin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 02-Jul-1998
 C:Accession: S62672
 R:Redosov, S.N.; Petersen, T.E.; Nexø, E.
 Biochim. Biophys. Acta 1292, 113-119, 1996
 A:Title: Transcobalamin from cow milk: Isolation and physico-chemical properties.
 A:Reference number: S62672; MUID:96139334
 A:Accession: S62672
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-26 <FED>
 C:Superfamily: gastric intrinsic factor

Query Match 24.8%; Score 26; DB 2; Length 26;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 5 LEFNLRLDALOK 19
 | | | : | | :
 Db 12 LVERLGGRLPXMDR 26

RESULT 14

S02788
 arylamine N-acetyltransferase (EC 2.3.1.5) 1 - human (fragments)
 C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 05-May-2000
 C:Accession: S02788
 R:Grant, D.M.; Lottspeich, F.; Meyer, U.A.
 FEBS Lett. 244, 203-207, 1989
 A:Title: Evidence for two closely related isozymes of arylamine N-acetyltransferase in h
 A:Reference number: S02788; MUID:89171260
 A:Accession: S02788
 A:Molecule type: protein
 A:Residues: 1-17; 18-26 <GRA>
 C:Keywords: acyltransferase; coenzyme A

Query Match 24.8%; Score 26; DB 2; Length 26;
 Best Local Similarity 38.5%; Pred. No. 1.8e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 10 LERLDALOKKLR 22
 | | | | : : : :
 Db 5 LEVLPDILETOIR 17

RESULT 15

A23691
 apolipoprotein C-I - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 31-Dec-1993
 C:Accession: A23691
 R:Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.
 J. Biol. Chem. 265, 22453-22459, 1990
 A:Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-migr
 ceptor-related protein.
 A:Reference number: A23691; MUID:91093092
 A:Accession: A23691
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-28 <WEI>
 C:Superfamily: apolipoprotein A-I
 C:Keywords: lipid binding; lipoprotein

Query Match 24.8%; Score 26; DB 2; Length 28;
 Best Local Similarity 30.0%; Pred. No. 2e+03;
 Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 LEFNLRLDALOKKLR 22
 | | | : | | : | : | :
 Db 7 LELPDKLEFGNTLEKAR 26

Search completed: November 20, 2001, 09:43:45
 Job time: 159 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:43:11 ; Search time 9.9 Seconds
(without alignments)
76.123 Million cell updates/sec

```
Title: US-08-940-096-146
Perfect score: 105
Sequence: 1 PVLELFENLLERLLDALQKKLK 22
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 1767

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Minimum DB seq length: 0
Maximum DB seq length: 30
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```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : SwissProt_39.*

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	31	29.5	21	1	CXGT_CONTO	P17684 conus tulip
2	31	29.5	30	1	END2_ONCKE	P01205 oncorhynch
3	29	27.6	19	1	NUO6_SOLTU	P80729 solanum tubu
4	28	26.7	13	1	TEME_RANTE	P56920 rana tempor
5	28	26.7	27	1	DMS4_PHYSA	P80280 rana tempor
6	26	24.8	28	1	APC1_RABIT	P33047 phyllomedus
7	26	24.8	30	1	V425_BORBU	P33047 oryctolagus
8	25	23.8	10	1	TEMC_RANTE	O51386 borrella bu
9	25	23.8	23	1	NIFD_ANAST	P56923 rana tempor
10	25	23.8	26	1	CT21_LITCI	P33177 anabaena sp
11	24	22.9	13	1	TEMC_RANTE	P81847 litorea cili
12	24	22.9	13	1	TEMD_RANTE	P56918 rana tempor
13	24	22.9	27	1	KT39_PICKL	P56919 rana tempor
14	24	22.9	27	1	SECR_SHEEP	P80326 pichia kluy
15	24	22.9	28	1	MAAL_RAT	P31299 ovis aries
16	23	21.9	11	1	UNO5_CLOPA	P57113 rattus norv
17	23	21.9	13	1	RPOC_MYCGA	P81350 clostridium
18	23	21.9	23	1	T2A_PARTE	P47716 mycoplasma
19	23	21.9	24	1	ACHB_ELEBL	O27173 parametium
20	23	21.9	26	1	VGLH_HSVF	P09689 electrophor
21	23	21.9	27	1	SECR_CANFA	P13160 feline herpi
22	23	21.9	27	1	SECR_RABIT	P09910 canis fami
23	23	21.9	28	1	CH60_MYCSM	P32647 oryctolagus
24	22	21.0	12	1	FREL_LITIN	P80673 mycobacteri
25	22	21.0	14	1	MAS1_VESLE	P82021 litorea infi
26	22	21.0	14	1	MAST_VESMA	P01214 vesputia lew
27	22	21.0	17	1	UC27_MAIZE	P04205 vespa manda
28	22	21.0	15	1	FLA2_BARBA	P80633 zea mays (m
29	22	21.0	21	1	BOH5_BOMVA	P350534 bartonella
30	22	21.0	21	1	BOH5_BOMVA	P82284 bombina var
31	22	21.0	24	1	CT31_LITCI	P82284 bombina var
32	22	21.0	26	1	ACHD_ELEBL	P81851 litorea cili
33	22	21.0	26	1	PUTA_KLEPN	P09691 electrophor
						P23725 klebsiella

34	22	21.0	27	1	PA55_CAP11	P80935	<i>capra hircu</i>
35	22	21.0	28	1	COB8_SOLU	P80499	<i>solanum tubu</i>
36	21.5	20.5	29	1	ATPA_BRWA	P26565	<i>bryopsis ma</i>
37	21	20.0	13	1	NEUT_CAVO	P32560	<i>cavia porce</i>
38	21	20.0	15	1	MC42_RHOV	P36870	<i>rhodococcus</i>
39	21	20.0	17	1	UP31_UPEIN	P82032	<i>uperoleia 1</i>
40	21	20.0	17	1	UP23_UPEIN	P82033	<i>uperoleia 1</i>
41	21	20.0	17	1	UP33_UPEIN	P82034	<i>uperoleia 1</i>
42	21	20.0	19	1	UP28_UPEMJ	P82040	<i>uperoleia m</i>
43	21	20.0	20	1	OAR_PHOY	P14803	<i>photinus py</i>
44	21	20.0	21	1	REV_HY2D2	P15830	<i>hunan immun</i>
45	21	20.0	22	1	UVSX_BP72	Q06727	<i>bacteriopho</i>

ALIGNMENTS

RESULT	1			
CXGT	CONTU	STANDARD:	PRT:	21 AA.
ID	CXGT_CONTU			
AC	P17684;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	CONANTOKIN-T (CON-T).			
OS	Conus tulipa (fish-hunting cone snail) (Tulip cone).			
OC	Euryptora; Metazoa; Mollusca; Gastropoda; Caenogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxID=6495;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=90202866; PubMed=2180933;			
RA	Haack J.A., Rivier J.E., Parks T.N., Mena E.E., Cruz L.J.,			
RA	Olivera B.M.;			
RT	"Conantokin-T. A gamma-carboxyglutamate containing peptide with			
RT	N-methyl-D-aspartate antagonist activity.";			
RL	J. Biol. Chem. 265:6025-6029(1990).			
RN	[2]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=97388301; PubMed=9247135;			
RA	Wardner S.E., Chen Z., Zhu Y., Porock M., Castellino F.J., Ni F.;			
RT	"The NMR solution structure of the NMDA receptor antagonist,			
RT	conantokin-T, in the absence of divalent metal ions.";			
RL	FEBS Lett. 411:19-26(1997).			
RN	[3]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=97153002; PubMed=8999936;			
RA	Skjaerbaek N., Nielsen K.J., Lewis R.J., Alewood P., Craik D.J.;			
RT	"determination of the solution structures of conantokin-G and			
RT	conantokin-T by CD and NMR spectroscopy.";			
RL	J. Biol. Chem. 272:2291-2299(1997).			
CC	-1- FUNCTION: INDUCES SLEEP-LIKE SYMPTOMS IN YOUNG MICE. INHIBITS			
CC	N-METHYL-D-ASPARTATE (NMDA) RECEPTOR-MEDIATED CALCIUM INFLUX IN			
CC	CENTRAL NERVOUS SYSTEM NEURONS.			
CC	PDB: A35225; A35225.			
DR	PDB: 1ON7; 04-SEP-97.			
KW	Venom; Vitamin K; Gamma-carboxyglutamic acid; Calcium; Amidation;			
KW	3D-structure.			
FT	MOD_RES	3	3	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	4	4	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	10	10	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	14	14	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	21	21	AMIDATION.
QO	SEQUENCE	21 AA;	2509 MW;	7F7B893AC4842C38 CRC64;

Query Match	29.5%;	Score 31;	DB 1;	Length 21;
Best Local Similarity	41.2%;	Pred. NO.	1.4e+02;	
Matches	7;	Conservative	4;	Mismatches 6; Indels 0; Gaps 0
OY	4	ELFENLERLLDALOK	20	
	:: :: :: :			


```

Query Match      26.7%  Score 28; DB 1; Length 27;
Best Local Similarity 41.2%  Pred. No. 4.8e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 5 LFEFNLRLDLALOKKL 21
    :|:::|::|
Db 2 LWMPLKRLKRAAKAL 18

RESULT 6
APCI_RABIT STANDARD: PRT: 28 AA.
AC P33047;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE APOLIPOPROTEIN C-I (Apo-CI) (FRAGMENT).
GN APOC1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=91093092; PubMed=2266137;
RA Weisgraber K.H., Mahley R.W., Kowal R.C., Hertz J., Goldstein J.L.,
RA Brown M.S.;
RT "Apolipoprotein C-I modulates the interaction of apolipoprotein E
RT with beta-migrating very low density lipoproteins (beta-VLDL) and
RT inhibits binding of beta-VLDL to low density lipoprotein
RT receptor-related protein.*"
RL J. Biol. Chem. 265:22453-22459(1990).
CC -1- FUNCTION: APPEARS TO MODULATE THE INTERACTION OF APOE WITH BETA-
CC MIGRATING VLDL AND INHIBIT BINDING OF BETA-VLDL TO THE LDL
CC RECEPTOR-RELATED PROTEIN.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -1- SIMILARITY: BELONGS TO THE APOC1 FAMILY.
DR PIR: A23691; A23691.
DR HSSP: P02654; 10PP.
KW Plasma; Lipid transport; VLDL.
FT NON_PEP 28
FT SEQUENCE 28 AA; 3165 MW; 2903C027F676541C CRC64;

Query Match      24.8%  Score 26; DB 1; Length 28;
Best Local Similarity 30.0%  Pred. No. 9.3e+02;
Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 LFEFNLRLDLALOKKL 22
    ||::|::|
Db 7 LELIPDKLKEGNTLEKAR 26

RESULT 7
Y425_BORBU STANDARD: PRT: 30 AA.
AC 051386;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHEICAL PROTEIN BB0425.
GN BB0425.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sulton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

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RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uiterback T., Wathey L., McDonald L., Atliach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi*."
RL Nature 390:580-586(1997).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE001147; AAC66799.1; -
DR TIGR: BB0425; -
KW Hypothetical protein.
SQ SEQUENCE 30 AA; 3688 MW; FF79F03D0ACCCEB4 CRC64;

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Query Match      24.8%  Score 26; DB 1; Length 30;
Best Local Similarity 50.0%  Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 11 ERLDLALOKKL 22
    :|||::|
Db 19 QNLTLPLNKKIK 30

RESULT 8
TEMP_RANFE STANDARD: PRT: 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TEMPORIN K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria*."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE BREVETININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1123 MW; 390549B37272457 CRC64;

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Query Match      23.8%  Score 25; DB 1; Length 10;
Best Local Similarity 60.0%  Pred. No. 4.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 LFEFNLRL 14
    |::|::|
Db 1 LPLNKLKSL 10

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RESULT 9
NIFD_ANASL STANDARD: PRT: 23 AA.
AC NIFD_ANASL
P31177;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1)
DE (NITROGENASE COMPONENT 1) (DINITROGENASE) (FRAGMENT).
GN NIFD.
NC Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=29412;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=93144353; PubMed=8424961;
RA Murphy S.T., Jackman D.M., Mulligan M.E.;
RT "Cloning and nucleotide sequence of the gene for dinitrogenase
reductase (nifH) from the heterocyst-forming cyanobacterium Anabaena
sp. L31."
RL Biochim. Biophys. Acta 1171:337-340(1993).
CC -1- FUNCTION: THE KEY ENZYMOLOGICAL REACTIONS IN NITROGEN FIXATION ARE
CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CC -1- CATALYTIC ACTIVITY: 8 REDUCED FERREDOXIN + 8 H(+) + N(2) + 16 ATP
= 8 OXIDIZED FERREDOXIN + 2 NH(3) + 16 ADP + 16 ORTHOPHOSPHATE.
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
30-32 FE, 2 MO, AND INORGANIC SULFUR.
CC -1- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
CC -----
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CC -----
EMBL: L04499; AAA22015.1; -
DR PIR: S28191; S28191.
DR InterPro: IPR000318; -
DR PROSITE: PS00090; NITROGENASE_1_2; PARTIAL.
DR PROSITE: PS00699; NITROGENASE_1_1; PARTIAL.
KW Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
FT NON TER 23
FT SEQUENCE 23 AA: 2666 MW: 9F2C70302E167806 CRC64;
OY 7 ENLEERLLDALOKKIK 22
DB 7 KNLYDENKELIOEVLR 22

Query Match 23.8%; Score 25; DB 1; Length 23;
Best Local Similarity 31.2%; Pred. No. 1e+03;
Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 7 ENLEERLLDALOKKIK 22
DB 7 KNLYDENKELIOEVLR 22

RESULT 10
CT21_LITCI STANDARD: PRT: 26 AA.
ID CT21_LITCI
P81847; P81848; P81849; P81850;
AC P81847; P81848; P81849; P81850;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CITROPIN 2.1.3 [CONTAINS: CITROPIN 2.1.2; CITROPIN 2.1.1; CITROPIN
2.1].
DE Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
NC NCBI_TaxID=94770;
OX [1]
RN [1]
RP SEQUENCE.

```

```

RC TISSUE=Skin;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Mahlitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RA Wallace J.C., Tyler M.J.;
RT "Host defence peptides from the skin glands of the Australian blue
mountains tree-frog Litoria citropa. Solution structure of the
antibacterial peptide citropin 1.1."
RL Eur. J. Biochem. 265:627-637(1999).
CC -1- TISSUE SPECIFICITY: DORSAL AND SUBVENTRAL SKIN GLANDS.
FT PEPTIDE 1 22 CITROPIN 2.1.
FT PEPTIDE 1 23 CITROPIN 2.1.1.
FT PEPTIDE 1 25 CITROPIN 2.1.2.
FT PEPTIDE 1 26 CITROPIN 2.1.3.
FT SEQUENCE 26 AA: 2519 MW: 7490C28EB2E4899A CRC64;
OY 13 LLDALOKKIK 22
DB 14 LVDLKPKIK 23

Query Match 23.8%; Score 25; DB 1; Length 26;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 13 LLDALOKKIK 22
DB 14 LVDLKPKIK 23

RESULT 11
TEND_RANTE
ID TEND_RANTE STANDARD: PRT: 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TEMPORIN C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
NC NCBI_TaxID=8407;
OX [1]
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
BACTERIA.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GABGURIN/RUGOSIN
FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD RES 13 13 AMIDATION.
FT SEQUENCE 13 AA: 1363 MW: 2201403A655B2448 CRC64;
OY 2 VLLEFENLEERLL 14
DB 1 LLLPLGNLNGLL 13

Query Match 22.9%; Score 24; DB 1; Length 13;
Best Local Similarity 46.2%; Pred. No. 7.8e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 VLLEFENLEERLL 14
DB 1 LLLPLGNLNGLL 13

RESULT 12
TEND_RANTE
ID TEND_RANTE STANDARD: PRT: 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TEMPORIN D.

```


OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RN NCBI_TaxID=8407;
 RP SEQUENCE AND SYNTHESIS.
 RC TRISSUE=SKIN.
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simeco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 Barra D.;
 RT "Temporaria", antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 KW Amphibian skin; Amidation; Multigene family.
 FT MOD.RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA: 1379 MW: 3EF35DFA65B2448 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 13;
 Best Local Similarity 46.2%; Pred. No. 7.8e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 2 VFLEFENLERLL 14
 DB 1 LPEIVGNLNSLL 13

RESULT 13
 KT39_PICCKL STANDARD; PRT; 27 AA.
 AC P80326;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE KILLER TOXIN KT395 (FRAGMENT).
 OS Pichia kluyveri (yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Pichia.
 RN NCBI_TaxID=36015;
 RP SEQUENCE.
 RC STRAIN=ATCC 66811 / GBS 7145;
 RA Martin C., Leis W., Radler F.;
 RL J. Gen. Appl. Microbiol. 40:0-0(1994).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 KW Toxin.
 FT NON-TER 27 27
 SQ SEQUENCE 27 AA: 3084 MW: CD935E165129E42A CRC64;

Query Match 22.9%; Score 24; DB 1; Length 27;
 Best Local Similarity 44.4%; Pred. No. 1.7e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 7 ENLEERLLD 15
 DB 16 ENLAQOQFVD 24

RESULT 14
 SECR_SHEEP STANDARD; PRT; 27 AA.
 AC P31299;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE SECRETIN.
 CC SCT.
 KW Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN NCBI_TaxID=9940;
 RP SEQUENCE.
 RC TRISSUE=Small intestine;
 RX MEDLINE=91239834; PubMed=2034821;
 RA Bouajoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
 Christophe J.;
 RT Purification and amino acid sequence of vasoactive intestinal
 RT peptide, peptide histidine isoleucineamide and secretin from the ovine
 RT small intestine.";
 RL Regul. Pept. 32:169-179(1991).
 CC -1- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
 CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
 CC BY THE STOMACH.
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR HSSP; P01274; 16CN.
 DR InterPro; IPR000532; .
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone; Amidation.
 FT MOD.RES 27 27 AMIDATION.
 SQ SEQUENCE 27 AA: 3056 MW: 2D4015814ED05B78 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 27;
 Best Local Similarity 42.1%; Pred. No. 1.7e+03;
 Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;
 OY 6 FENLEERLLDA--LQKKLK 22
 DB 6 FTSELSRLDSARLRLIQ 24

RESULT 15
 MAAL_RAT STANDARD; PRT; 28 AA.
 AC P57113;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALEYLACETOACETATE ISOMERASE (EC 5.2.1.2) (MAAL) (GLUTATHIONE S-
 DE TRANSFERASE ZETA 1) (EC 2.5.1.18) (GSTZ1-1) (FRAGMENT).
 GN GSTZ1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RP SEQUENCE AND CHARACTERIZATION.
 RC STRAIN=FISCHER 344; TRISSUE=Liver;
 RX MEDLINE=98198370; PubMed=9531472;
 RA Tong Z., Board P.G., Anders M.W.;
 RT "Glutathione transferase zeta catalyses the oxygenation of the
 RT carcinogen dichloroacetic acid to glyoxylic acid".
 RL Biochem. J. 331:371-374(1998).
 CC -1- FUNCTION: PROBABLE BIFUNCTIONAL ENZYME SHOWING MINIMAL
 CC GLUTATHIONE-CONJUGATING ACTIVITY WITH ETHACRYNIC ACID AND 7-
 CC CHLORO-4-NITROBENZ-2-OXA-1, 3-DIAZOLE AND MALEYLACETOACETATE
 CC ISOMERASE ACTIVITY. HAS ALSO LOW GLUTATHIONE PEROXIDASE ACTIVITY
 CC WITH T-BUTYL AND CUMENE HYDROPEROXIDES (BY SIMILARITY). IS ABLE TO
 CC CATALYZE THE GLUTATHIONE DEPENDENT OXYGENATION OF DICHLOROACETIC
 CC ACID TO GLYOXYLIC ACID.
 CC -1- CATALYTIC ACTIVITY: 4-MALEYLACETOACETATE = 4-FUMARYLACETOACETATE.
 CC -1- CATALYTIC ACTIVITY: RX + GLUTATHIONE = HX + R-S-G.
 CC -1- COFACTOR: THE MAAL ACTIVITY REQUIRES GLUTATHIONE (BY SIMILARITY).
 CC -1- PATHWAY: CATABOLISM OF TYROSINE; FOURTH STEP, CATABOLISM OF
 CC PHENYLALANINE; FIFTH STEP.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOSOLPLASMIC.
CC -1- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY, ZETA FAMILY.
KW Isomerase; Transferase; Multifunctional enzyme;
KW Phenylalanine catabolism; Tyrosine catabolism.
FT NON_TER 1 28
FT NON_TER 1 28
SQ SEQUENCE 28 AA; 2943 MW; 1070608C44491C25 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 28;
Best Local Similarity 38.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 NLERLDALQKK 20
| | | | | : |
DB 10 NALDKTIQSTAGK 22

Search completed: November 20, 2001, 09:45:52
Job time: 161 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:43:26 ; Search time 20.8 seconds

(without alignments)
139.938 Million cell updates/sec

Title: US-08-940-096-146

Perfect score: 105

Sequence: 1 PYLELEFENLERLDAIQKLLK 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 11509

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREML16:
1: sp-archaea:
2: sp-bacteria:
3: sp-fungi:
4: sp-human:
5: sp-invertebrate:
6: sp-mammal:
7: sp-mhc:
8: sp-organelle:
9: sp-phage:
10: sp-plant:
11: sp-rodent:
12: sp-unclassified:
13: sp-vertebrate:
14: sp-virus:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	33.3	26	2	025285
2	34	32.4	30	2	0918X1
3	34	32.4	30	2	0918W9
4	33	31.4	20	9	036458
5	31.5	30.0	29	4	090KSO
6	31	29.5	23	11	09JIND
7	29	27.6	20	13	09PS63
8	29	27.6	27	13	P82847
9	28	26.7	15	11	090U25
10	28	26.7	16	6	09TRR2
11	28	26.7	25	14	036582
12	28	26.7	25	14	036585
13	28	26.7	25	14	036588
14	28	26.7	25	14	036591
15	28	26.7	25	14	036594
16	28	26.7	25	14	036597
17	28	26.7	27	14	09W7S6
18	28	26.7	29	11	P97599
19	28	26.7	29	14	092646

20	28	26.7	29	14	092648	092648 hepatitis e
21	28	26.7	30	14	09WLK3	09WLK3 hepatitis e
22	27	25.7	13	13	P82881	P82881 rana clamit
23	27	25.7	19	2	09R4T9	09R4T9 bacillus th
24	27	25.7	22	8	P92621	P92621 cirotatus vi
25	27	25.7	24	13	09PR22	09PR22 amia calva
26	27	25.7	29	6	09XS75	09XS75 sus scrofa
27	27	25.7	30	11	09QV95	09QV95 cavia (quin
28	26	24.8	12	2	053183	053183 rhodococcus
29	26	24.8	16	4	09UCY4	09UCY4 homo sapien
30	26	24.8	17	2	09R5X6	09R5X6 mycoplasma
31	26	24.8	20	8	09Z7Y4	09Z7Y4 mirax sp. c
32	26	24.8	23	13	P82398	P82398 litoria ran
33	26	24.8	23	13	P82400	P82400 litoria ran
34	26	24.8	24	13	P82838	P82838 rana berlan
35	26	24.8	26	6	09TR25	09TR25 bos taurus
36	26	24.8	27	5	09Y182	09Y182 priapulid c
37	26	24.8	29	5	025603	025603 onchocerca
38	26	24.8	21	11	008923	008923 mus musculu
39	25.5	24.3	23	6	09TR81	09TR81 sus scrofa
40	25	23.8	24	4	09UNM2	09UNM2 homo sapien
41	25	23.8	25	4	09UED3	09UED3 homo sapien
42	25	23.8	26	2	09F625	09F625 staphylococ
43	25	23.8	26	13	P82069	P82069 litoria gen
44	25	23.8	26	3	09U799	09U799 schizosacch
45	25	23.8	28	3	09U799	09U799 schizosacch

ALIGNMENTS

RESULT 1
ID 025285 PRELIMINARY: PRT: 26 AA.
AC 025285;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOPHETICAL 3.2 KDA PROTEIN.
GN HP0560 OR JHP0507.
OS Helicobacter pylori (Campylobacter pylori), and
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group.
OC Helicobacter.
OX NCBI_TaxID=210, 85963;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA McIneney K., Fitzgerald D., Dodson R., Khalak H.G., Glodek A.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Mallin E.,
RA Hayes W.S., Borodovsky M., Karpi P.D., Smith H.O., Fraser C.M.,
RT Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=99120557; PubMed=9923682;
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Tamplin P.J., Noonan B., Guille B.C., deJonghe B.L., Carmel G.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).

DR EMBL: AE000570; AAD07633.1; -
 DR EMBL: AE001484; AAD06083.1; -
 DR TIGR: HP0507; -
 DR TIGR: HP0560; -
 KW Hypothetical protein.
 SC SEQUENCE 26 AA; 3169 MW; 34FE239BE3139AA1 CRC64;

Query Match 33.3%; Score 35; DB 2; Length 26;
 Best Local Similarity 58.3%; Pred. No. 4e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 ERLDLDALQK 20
 DB 15 LLYRLDVLQK 26

RESULT 2
 Q9L8X1 PRELIMINARY; PRT; 30 AA.

AC Q9L8X1:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 15, last annotation update)
 DE POLYKETIDE SYNTHASE MODULE 6 (FRAGMENT).
 OS Streptomyces venezuelae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=54571;

RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC15068;
 RX MEDLINE=20179700; PubMed=10713461;
 RA Xue Y., Wilson D., Sherman D.H.;
 RT "Genetic architecture of the polyketide synthases for methymycin and pikromycin series macrolides.";
 RL Gene 245:203-211(2000).
 DR EMBL: AF193251; AAF61860.1; -
 FT NON_TER 30
 SQ SEQUENCE 30 AA; 3562 MW; 673D2569873325A3 CRC64;

Query Match 32.4%; Score 34; DB 2; Length 30;
 Best Local Similarity 58.3%; Pred. No. 6.3e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 ERLDLDALQK 22
 DB 6 EQLVDALRASLK 17

RESULT 3
 Q9L8W9 PRELIMINARY; PRT; 30 AA.

AC Q9L8W9:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 15, last annotation update)
 DE POLYKETIDE SYNTHASE MODULE 6 (FRAGMENT).
 OS Streptomyces narbonensis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=67333;

RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19790;
 RX MEDLINE=20179700; PubMed=10713461;
 RA Xue Y., Wilson D., Sherman D.H.;
 RT "Genetic architecture of the polyketide synthases for methymycin and pikromycin series macrolides.";
 RL Gene 245:203-211(2000).
 DR EMBL: AF193252; AAF61862.1; -
 FT NON_TER 30
 SQ SEQUENCE 30 AA; 3562 MW; 673D2569873325A3 CRC64;

SQ SEQUENCE 30 AA; 3562 MW; 673D2569873325A3 CRC64;

Query Match 32.4%; Score 34; DB 2; Length 30;
 Best Local Similarity 58.3%; Pred. No. 6.3e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 ERLDLDALQK 22
 DB 6 EQLVDALRASLK 17

RESULT 4
 Q38458 PRELIMINARY; PRT; 20 AA.

AC Q38458:
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 OS Bacteriophage phi-105.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 OX NCBI_TaxID=10717;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86056972; PubMed=3934047;
 RA Cully D.F., Garro A.J.;
 RT "Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage phi 105: identification of the repressor gene and its

RT mRNA and protein products.";
 RL Gene 38:153-164(1985).
 DR EMBL: M11920; AAA8402.1; -
 KW Hypothetical protein.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2342 MW; FCE3D10864EB54AA CRC64;

Query Match 31.4%; Score 33; DB 9; Length 20;
 Best Local Similarity 50.0%; Pred. No. 5.7e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 FENLERLDALQK 19
 DB 6 FEOLMAETKQALQK 19

RESULT 5
 Q9UKS0 PRELIMINARY; PRT; 29 AA.

AC Q9UKS0:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, last annotation update)
 DE NUP98-RAP1GDS1 FUSION PROTEIN TYPE 2 (FRAGMENT).
 GN NR62.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;

RN (1)
 RP SEQUENCE FROM N.A.
 RA Hussey D.J., Nicola M., Moore S., Dobrovic A.;
 RT "The (4;11)(q21;p15) translocation fuses the NUP98 and RAP1GDS1 genes and is recurrent in T cell acute lymphocytic leukemia.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF133333; AAD54077.1; -

FT NON_TER 1
 SQ SEQUENCE 29 AA; 2970 MW; A68E5D45DDCB205F CRC64;

Query Match 30.0%; Score 31.5; DB 4; Length 29;


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RESULT 10
O9TRA2 PRELIMINARY; PRT; 16 AA.
ID 09TRA2:
AC 09TRA2:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TROPOMYOSIN (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=95029805; PubMed=7943254;
RA Rao U.J., Denslow N.D., Block E.R.;
RT "Hypoxia induces the synthesis of tropomyosin in cultured porcine
pulmonary artery endothelial cells."
RL Am. J. Physiol. 267:R271-R281(1994).
SQ SEQUENCE 16 AA; 1950 MW; E042C558DEA778D CRC64;

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Query Match 26.7%; Score 28; DB 6; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.1e+03;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 14 LDALQKRLK 22
:|::|::|:
DB 1 MDALKKKKMO 9

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RESULT 11
O36582 PRELIMINARY; PRT; 25 AA.
ID 036582:
AC 036582:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ORF-1 (FRAGMENT).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIRGIZIA (OSH);
RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.,
Purcell R.;
RL J. Med. Virol. 0:0-0(1997).
DR EMBL; AF010417; AAB65529.1; -.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2772 MW; 5B7D6EC036BBF038 CRC64;

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Query Match 26.7%; Score 28; DB 14; Length 25;
Best Local Similarity 46.2%; Pred. No. 3.2e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 PVLELFENLRL 13
|||:|::|:
DB 12 PVLDLTNSILCRV 24

```

RESULT 12

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O36585 PRELIMINARY; PRT; 25 AA.
ID 036585:
AC 036585:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ORF-1 (FRAGMENT).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=12461;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOROCCO/F12;
RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.,
Purcell R.;
RL J. Med. Virol. 0:0-0(1997).
DR EMBL; AF010418; AAB65532.1; -.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2772 MW; 5B7D6EC036BBF038 CRC64;

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Query Match 26.7%; Score 28; DB 14; Length 25;
Best Local Similarity 46.2%; Pred. No. 3.2e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 PVLELFENLRL 13
|||:|::|:
DB 12 PVLDLTNSILCRV 24

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RESULT 13
O36588 PRELIMINARY; PRT; 25 AA.
ID 036588:
AC 036588:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ORF-1 (FRAGMENT).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOROCCO/F13;
RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.,
Purcell R.;
RL J. Med. Virol. 0:0-0(1997).
DR EMBL; AF010419; AAB65535.1; -.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2772 MW; 5B7D6EC036BBF038 CRC64;

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Query Match 26.7%; Score 28; DB 14; Length 25;
Best Local Similarity 46.2%; Pred. No. 3.2e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 PVLELFENLRL 13
|||:|::|:
DB 12 PVLDLTNSILCRV 24

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RESULT 14
O36591 PRELIMINARY; PRT; 25 AA.
ID 036591:
AC 036591:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ORF-1 (FRAGMENT).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOROCCO/F23;
RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.,
Purcell R.;
RL J. Med. Virol. 0:0-0(1997).
DR EMBL; AF010420; AAB65538.1; -.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2772 MW; 5B7D6EC036BBF038 CRC64;

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Query Match 26.7%; Score 28; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 3.2e+03;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 1 PVLLEFENLIERL 13
 |||:|::|:|:
 Db 12 PVLDTJNSILCRV 24

RESULT 15
 036594
 ID 036594; PRELIMINARY; PRT; 25 AA.
 AC 036594;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE ORF-1 (FRAGMENT).
 OS Hepatitis E virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage.
 OX NCBI_TaxID=12461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUNISIA;
 RA Chatterjee R.; Tsarev S., Pilot J., Coursaget P., Emerson S.,
 RA Purcell R.;
 RL J. Med. Virol. 0:0-0(1997).
 DR EMBL; AF010421; AAB66541.1; -.
 FT NON_TER 1
 SO SEQUENCE 25 AA; 2786 MW; B7AD6EC036BFF020 CRC64;

Query Match 26.7%; Score 28; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 3.2e+03;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 1 PVLLEFENLIERL 13
 |||:|::|:|:
 Db 12 PVLDTJNSILCRV 24

Search completed: November 20, 2001, 09:46:20
 Job time: 174 sec

